

## SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science and Technology

<120> A GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase  
Gene From Arabidopsis Thaliana and Method for Producing  
A GDP-fucose Using Thereof

<130> PH-935-PCT

<150> JP 11-329045

<151> 1999-11-19

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 312

<212> PRT

<213> Arabidopsis thaliana

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Met Ser Asp Lys Ser Ala Lys Ile Phe Val Ala Gly His Arg Gly Leu

1

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Val Gly Ser Ala Ile Val Arg Lys Leu Gln Glu Gln Gly Phe Thr Asn

20

25

30

Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp

35

40

45

Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala

50

55

60

Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp

65

70

75

80

Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala

85

90

95

Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile

100

105

110

Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr

115

120

125

Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala

130

135

140

Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala

145

150

155

160

Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His

165

170

175

Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu

180

185

190

Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser

195

200

205

Pro Leu Arg Glu Phe Leu His Val Asp Asp Leu Ala Asp Ala Cys Val

210

215

220

Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser

225

230

235

240

Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val

245

250

255

Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly

260

265

270

Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp

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Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp

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Tyr Leu Lys Asn Val Cys Asn Arg

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<211> 936

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gtt gga tct gcc att gtc cgc aag ctt cag gaa caa ggt ttc acc aat	96	
Val Gly Ser Ala Ile Val Arg Lys Leu Gln Glu Gln Gly Phe Thr Asn		
20	25	30

ctc gtt ctt aaa aca cac gcc gag ctt gat ctc act cgt caa gcc gat	144	
Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp		
35	40	45

gtt gaa tcc ttc ttt tct caa gag aag cca gtt tat gta atc cta gca	192	
Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala		
50	55	60

gca gct aaa gtt ggt ggt att cac gct aac aac acc tat cct gct gat	240		
Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp			
65	70	75	80

ttc att ggt gtc aat ctc cag att cag acc aat gtg atc cac tct gca	288
Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala	

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95

tat gag cac ggt gtg aag aag ctt ctc ttc ctt gga tca tcc tgc att 336

Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile

100

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tac cct aaa ttt gct cct cag cca att cct gag tct gct ttg tta aca 384

Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr

115

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gca tcg ctt gaa cca act aat gag tgg tat gct att gct aag atc gct 432

Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala

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ggg att aag act tgt cag gct tat agg att cag cac gga tgg gat gca 480

Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala

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atc tct ggc atg cct act aat ctc tat ggt cct aat gac aat ttc cac 528

Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His

165

170

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ccg gag aat tct cat gtg ctt cct gct ctt atg agg agg ttc cac gag 576

Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu

180

185

190

gcg aaa gtg aat gga gcg gag gaa gtt gtg gtg tgg ggt aca ggt agt 624

Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser

195

200

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 210 215 220

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 Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser  
 225 230 235 240

ggt caa gaa gtg act att aga gag ttg gct gag ttg gtg aaa gag gtt 768  
 Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val  
 245 250 255

gtt ggt ttt gaa ggg aag ctt gga tgg gat tgc act aag cca gat ggc 816  
 Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly  
 260 265 270

aca ccg agg aaa ctt atg gac agc tca aag ctc gcg tct ttg ggt tgg 864  
 Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp  
 275 280 285

aca cct aag gtt tct ctt aga gat ggt ctg agc caa act tat gat tgg 912  
 Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp  
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tat ttg aag aat gtt tgc aac cga 936  
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<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<210> 6

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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